

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 13, 2001, 13:34:05 ; Search time 57.85 Seconds

(without alignments)
312.059 Million cell updates/sec

Title: US-09-784-340-2

Perfect score: 1 MRSKSLVFLVLLDLPFCVGC.....KCFIFSCQFKFKTKIEKRE 527

Sequence: 2802

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt_39:*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1732	61.8	530	1	UDBH_HUMAN
2	1729	61.7	528	1	UDBH_HUMAN
3	1713	61.1	530	1	UDBH_HUMAN
4	1712	61.1	528	1	UDBJ_MACFA
5	1691.5	60.4	527	1	UDAL_RAT
6	1686	60.2	530	1	UDBK_MACFA
7	1685	60.1	529	1	UDBI_RAT
8	1676.5	59.8	529	1	UDBI_HUMAN
9	1668.5	59.5	530	1	UDBE_RABIT
10	1661.5	59.3	529	1	UDB9_MACFA
11	1648	58.8	531	1	UDBD_RABIT
12	1635.5	58.4	528	1	UDBA_HUMAN
13	1628.5	58.1	529	1	UDBB_HUMAN
14	1620	57.8	502	1	UDCL_RABIT
15	1595	56.9	530	1	UDBC_RAT
16	1587	56.6	530	1	UDBG_RABIT
17	1580	56.4	530	1	UDBE_RAT
18	1572	55.6	530	1	UDBE_MOUSE
19	1557	55.1	530	1	UDBE_MOUSE
20	1556	55.5	530	1	UDB3_RAT
21	1499	53.5	530	1	UDBE_RAT
22	1137	40.6	533	1	UD11_HUMAN
23	1128.5	40.3	533	1	UD12_RAT
24	1124.5	40.1	531	1	UD15_RAT
25	1122.5	40.1	535	1	UD11_MOUSE
26	1109	39.6	535	1	UD11_MOUSE
27	1097.5	39.2	533	1	UD12_MOUSE
28	1096.5	39.1	530	1	UD12_HUMAN
29	1094.5	39.1	531	1	UD13_RAT
30	1092	39.0	531	1	UD16_MOUSE
31	1081.5	38.6	534	1	UD13_HUMAN
32	1077	38.4	531	1	UD16_HUMAN
33	1076.5	38.4	534	1	UD14_HUMAN

ALIGNMENTS

RESULT	ID	UDBH_HUMAN	STANDARD	PRT	530 AA.
AC	075795				
DT	15-DEC-1998 (Rel. 37, Created)				
DT	15-DEC-1998 (Rel. 37, Last sequence update)				
DT	15-DEC-1998 (Rel. 37, Last annotation update)				
DE	UDP-GLUCURONOSYLTRANSFERASE 2B17 PRECURSOR, MICROSOFT (EC 2.4.1.17)				
DE	(UDPCT) (C19-STEROID SPECIFIC UDP-GLUCURONOSYLTRANSFERASE).				
GN	UGT2B17				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Prostate;				
RX	MEDLINE=96394358; PubMed=8798464;				
RA	Beaulieu M., Levesque E., Hum D.W., Belanger A.;				
RT	Isolation and characterization of a novel cDNA encoding a human				
RT	UDP-glucuronosyltransferase active on C19 steroids.";				
J	Biol. Chem. 271:22855-22862(1996).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=98030207; PubMed=9364925;				
RA	Beaulieu M., Levesque E., Tchernof A., Beatty B.G., Belanger A.;				
RT	Hum D.W.;				
RT	"Chromosomal localization, structure, and regulation of the UGT2B17				
RT	gene, encoding a C19 steroid metabolizing enzyme.";				
RL	DNA Cell Biol. 16:1143-1154(1997).				
CC	-1- FUNCTION: UDPGT IS OF MAJOR IMPORTANCE IN THE CONJUGATION AND				
CC	SUBSEQUENT ELIMINATION OF POTENTIALLY TOXIC XENOBIOTICS AND				
CC	ENDOGENOUS COMPOUNDS. THE MAJOR SUBSTRATES OF THIS ISOZYME ARE				
CC	EUGENOL > 4-METHYLMETHYLTERPENE > DIHYDROTESTOSTERONE (DHT) >				
CC	ANDROSTERONE (ADT).				
CC	ANDROSTERONE (ADT).				
CC	CATALYTIC ACTIVITY: UDP-GLUCURONATE + ACCEPTOR -> UDP + ACCEPTOR				
CC	BETA-D-GLUCURONOSIDE.				
CC	-1- SUBCELLULAR LOCATION: MICROSOFT.				
CC	-1- TISSUE SPECIFICITY: EXPRESSED IN VARIOUS TISSUES INCLUDING THE				
CC	LIVER, KIDNEY, TESTIS, UTERUS, PLACENTA, MAMMARY GLAND, ADRENAL				
CC	GLAND, SKIN, AND PROSTATE.				
CC	-1- SIMILARITY: BELONGS TO THE UDP-GLYCOSYLTRANSFERASE FAMILY.				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration				
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -				
CC	the European Bioinformatics Institute. There are no restrictions on its				
CC	use by non-profit institutions as long as its content is in no way				
CC	modified and this statement is not removed. Usage by and for commercial				
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/				
CC	or send an email to license@isb-sib.ch).				
DR	EMBL: U59209; AAC25491.1; -				
DR	MIM: 601903; -				
DR	InterPro: IPR002213; -				
DR	Pfam: PF00201; UDPGT. 1.				

DR PROSITE: PS00375; UDEGT; 1.
 KM Transferrase; Glycosyltransferase; Glycoprotein; Transmembrane; Signal;
 KW Multigene family; Microsome.
 FT SIGNAL 1 23
 FT CHAIN 24 530
 FT TRANSMEM 495 515
 FT CARBOHYD 65 65
 FT CARBOHYD 316 316
 FT CARBOHYD 483 483
 SQ SEQUENCE 530 AA; 61095 MW; 8E59EB643CF43760 CRC64;

Query Match
 Best Local Similarity 61.8%; Score 1732; DB 1; Length 530;
 Matches 326; Conservative 74; Mismatches 112; Indels 18; Gaps 3;

OY 9 VELLQLQFC-VCCGFCGKVLVPCDMSHLNKKVILEELIVGHEVTVLTHSKPSLIDYR 67
 DB 8 VELLQLQFCVSSGCGKVLVPTFESHMINNKITLLELVGHEVTVLTHSKPSLIDYR 67
 OY 68 KPSAKFEVYHMPDRTENEELFVDLAINVLPGLSTWOSVILNDFEYVIRCTLMK---- 123
 DB 68 KSSAKILEVYPTSLTKNLEDEFFMKM-----FDRWYTSISKNTFMVSFSLQELCWEY 120
 OY 124 -----KCESFIYNOTLKKKLOETMYDMLIDPVIPCDLMAELLAVPPVLTIRISVGN 177
 DB 121 SDYNIKICEADVANKKMKRKQESKFVDVLADVAPCGELAEELNIFLYSLRFSVGYT 180
 OY 178 MERCGKIPAEVLVYPVPMGLTDMPLELVKNSMLSVLFHFYIODYDYHFWFEFYKA 237
 DB 181 VEKNGGGLFPSPVYVPMSELSDQIMFERIKMITYLVYDFEFOAVDLKKMOFSEV 240
 OY 238 LGRTTTCETVYGAKEIMLIRYMPDEFFPOPPVNFYVGGSLCKPAAKALPKEMENVOSS 297
 DB 241 LGRTTTEFTMGKEMMLIRYMPDEFFPRPLPVNDVGVGHCKPAPKPLPEMEFEVOSS 300
 OY 298 GEDGIVFSGSLFQNTYEERKANTIASALAOIPQKVLRRKKGKPSLTGANTRIYDIPQ 357
 DB 301 GENGIYVESIGSMISNSESANMIASALAOIPQKVLRRDGGKPNLGSNTRLYKWLPO 360
 OY 358 NDLLGHKTKAFTTHGMCNFIYEAHYGVPMGVPIFGDLDNIAHKAAGAWEINEKT 417
 DB 361 NDLLGHKTKAFTTHGTCNFIYEAHYGVPMGVPIFGDLDNIAHKAAGAWEINEKT 420
 OY 418 MISEDLLRALRYITDSSYKENAMRLSRHHDPVKPLDAVWIEFVMMHKAHKAHRS 477
 DB 421 MSSRDLLNALKSVINDPYKENIMKLSRIHDDPVKPLDAVWIEFVMMHKAHKAHRS 480
 OY 478 AHDLTFQHSIDVIGFLFCVATAFLETKCFELSCQKFNKTRKTEKRE 527
 DB 481 AHDLTFQHSIDVIGFLFCVATAFLETKCFELSCQKFNKTRKTEKRE 530

RESULT 2
 UDB4_HUMAN STANDARD. PRT; 528 AA.
 AC P06133; P36538; O60731; O60867;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE UDE-GLUCURONOSYLTRANSFERASE 2B4 PRECURSOR, MICROSOMAL (EC 2.4.1.17)
 DE (UDEGT) (HYDROXYCHOLIC ACID) (HLUG25) (UDEGT-1).
 GN UGT2B4 OR UGT2B11.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OC NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE-87241362; PubMed-3109396;
 RA Jackson M.R., McCarthy L.R., Harding D., Wilson S., Coughtrie M.W.H.,
 Burchell B.;

RT "Cloning of a human liver microsomal UDP-glucuronosyltransferase
 RT cDNA.";
 RL Biochem. J. 242:581-588(1987).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE-93326164; PubMed-8333863;
 RA Jin C.-Y., Miners J.O., Lillywhite K.J., McKenzie P.I.;
 RT "cDNA cloning and expression of two new members of the human liver
 RT UDP-glucuronosyltransferase 2B subfamily.";
 RL Biochem. Biophys. Res. Commun. 194:496-503(1993).
 RN [3]
 RP SEQUENCE FROM N.A., AND VARIANT GLU-458.
 RA Levesque E., Beaulieu M., Belanger A.;
 RT UGT2B4(E458): a UDP-glucuronosyltransferase encoded by a polymorphic
 RT gene with differential substrate specificity.";
 RL Submitted (May-1998) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: UDEGT IS OF MAJOR IMPORTANCE IN THE CONJUGATION AND
 CC SUBSEQUENT ELIMINATION OF POTENTIALLY TOXIC XENOBIOTICS AND
 CC ENDOGENOUS COMPOUNDS. ACTIVE ON POLYHYDROXYLATED ESTROGENS (SUCH
 CC AS ESTRADIOL, 4-HYDROXYESTRONE AND 2-HYDROXYESTRADIOL) AND XENOBIOTICS
 CC (SUCH AS 4-METHYLBULBELLIFERONE, 1-NAPHTHOL, 4-NITROPHENOL,
 CC 2-AMINOPHENOL, 4-HYDROXYBIPHENYL AND MENTHOL).
 CC -1- FUNCTION: CAPABLE OF 6 ALPHA-HYDROXYGLUCURONIDATION OF
 CC HYDROXYCHOLIC ACID.
 CC -1- CATALYTIC ACTIVITY: UDP-GLUCURONATE + ACCEPTOR = UDP + ACCEPTOR
 CC BETA-D-GLUCURONOSIDE.
 CC -1- SUBCELLULAR LOCATION: MICROSOMAL.
 CC -1- SIMILARITY: BELONGS TO THE UDP-GLYCOSYLTRANSFERASE FAMILY.
 CC CAUTION: REF.2 THOUGHT THAT THIS WAS A NEW FORM (UGT2B11). THE
 CC NAME UGT2B11 HAS NOW BEEN REUSED FOR ANOTHER HUMAN ENZYME.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: Y00317; CAA68415.1; -
 CC EMBL: AF064200; AAC95002.1; -
 CC EMBL: AJ005162; CAA06396.1; -
 CC PIR: A27878; A27878.
 CC PIR: JN0619; JN0619.
 CC MIM: 600067; -
 DR InterPro: IPR002213; -
 DR Pfam: PF00201; UDEGT; 1.
 DR PROSITE: PS00375; UDEGT; 1.
 KW Transferrase; Glycosyltransferase; Glycoprotein; Transmembrane; Signal;
 KW Multigene family; Microsome; Polymorphism.
 FT SIGNAL 1 23
 FT CHAIN 24 528
 FT TRANSMEM 493 509
 FT CARBOHYD 315 315
 FT VARIANT 458 458
 FT
 FT CONFLICT 109 109 F->L (IN REF. 2).
 FT CONFLICT 171 172 SL->RP (IN REF. 1).
 FT CONFLICT 382 387 EAIYHG->KAISPR (IN REF. 1).
 FT CONFLICT 396 396 F->L (IN REF. 2).
 SQ SEQUENCE 528 AA; 60512 MW; 6B45E6769971A078 CRC64;

Query Match
 Best Local Similarity 61.7%; Score 1729; DB 1; Length 528;
 Matches 332; Conservative 61; Mismatches 131; Indels 4; Gaps 3;

OY 3 SDKSAVFLILQFC-VCCGFCGKVLVPCDMSHLNKKVILEELIVGHEVTVLTHSKP 61
 DB 2 SMKTSALLILQFCVSSGCGKVLVPTFESHMINNKITLLELVGHEVTVLTHSKP 61
 OY 62 SLIDYRRPALKFEVYHMPDRTENEELFVDLAIN--VLPLSTWOSVILNDFEYVIRG 119

DR	EMBL: AF112112; AAD24435.1; -.	
DR	InterPro: IPR002213; -.	
DR	Pfam: PF00201; UDPGT; 1.	
DR	PROSITE: PS00375; UDPGT; 1.	
KW	Transferase; Glycosyltransferase; Glycoprotein; Transmembrane; Signal.	
KW	MultiGene family; Microsome.	
FT	SIGNAL	1..21
FT	CHAIN	22..528
FT	TRANSMEM	493..513
FT	CARBOHYD	315..315
SO	SEQUENCE	528 AA; 60741 MW; 3BBD2AE714A27AEE CRC64.

100

02 11FDFNNPSELENEI--CPISLIEIE--FQDSVTQLVKRWSDIRKDTFWPHFLHVQEMMM 117

CONFIDENTIAL

00 236 KATADONTIANTHIA.....

QY 296 SSGEDIVFSLGSLFONVTEKANTASAJAOTPOKVIWPYKCYRDCMIGANEDRUEVIT 333

550 FUNDLGHFNKAF.IIHGGMNGLYEAIYHGVPMGVPIFGDQLDNI AHMKAKGA VEINF 415

4/5

[illegible]

JDA1_RAT

01-JUN-1994 (Rel. 29, Last sequence update)

OS *Rattus norvegicus* (Bat)

$$\begin{bmatrix} 1 \\ 1 \end{bmatrix}$$

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RESULT 4
ID      UDBJ_MACFA
AC      09XT55;
DT      30-MAY-2000 (Rel. 39, Created)
DT      30-MAY-2000 (Rel. 39, Last sequence update)
DT      30-MAY-2000 (Rel. 39, Last annotation update)
DE      UDP-GLUCURONOSYLTRANSFERASE 2B19 PRECURSOR, MICROSOMAL (EC 2.4.1.17).
GN      UGT2B19.
OS      Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC      Cercopithecinae; Macaca.
OX      NCBI_TaxId=9541;
OY      (1)
RN      SEQUENCE FROM N.A.
RP      TISSUE=Liver, and Prostate.
RX      MEDLINE=99203465; PubMed=10102998;
RA      Belanger G., Barbier O., Hum D.W., Belanger A.:
RT      "Molecular cloning, expression and characterization of a monkey
RT      steroid UDP-glucuronosyltransferase, UGT2B19, that conjugates
RT      testosterone.";
RL      Eur. J. Biochem. 260:701-708(1999).
CC      -1- FUNCTION: UDPGT IS OF MAJOR IMPORTANCE IN THE CONJUGATION AND
CC      SUBSEQUENT ELIMINATION OF POTENTIALLY TOXIC XENOBIOTICS AND
CC      ENDOGENOUS COMPOUNDS. THIS ISOZYME DISPLAYS ACTIVITY TOWARD
CC      SEVERAL CLASSES OF XENOBIOTIC SUBSTRATES: EUGENOL, 4-
CC      METHYLOUMBELLIFERONE, P-NITROPHENOL, 1-NAFTHOL, P,P'-BIPHENOL,
CC      NAFINEXENIN AND O,O'-BIPHENOL. ACTIVE ALSO ON 3A-HYDROXY AND 17B-
CC      HYDROXY POSITIONS OF STEROIDS.
CC      -1- FUNCTION: CONTRIBUTES TO THE FORMATION OF ANDROGEN GLUCURONIDE IN
CC      EXTRAHEPATIC STEROID TARGET TISSUES SUCH AS THE PROSTATE.
CC      -1- CATALYTIC ACTIVITY: UDP-GLUCURONATE + ACCEPTOR = UDP + ACCEPTOR
CC      BETA-D-GLUCURONOSIDE.
CC      -1- SUBCELLULAR LOCATION: MICROSOMAL (BY SIMILARITY).
CC      -1- TISSUE SPECIFICITY: EXPRESSED IN LIVER, OVARY, PROSTATE, COLON,
CC      KIDNEY, PANCREAS, BRAIN, CEREBELLUM, MAMMARY GLAND AND EPIDIDYMS.
CC      NOT EXPRESSED IN SMALL INTESTINE, SPLEEN, BLADDER, ADRENAL GLAND
CC      AND TESTIS.
CC      -1- SIMILARITY: BELONGS TO THE UDP-GLYCOSYLTRANSFERASE FAMILY.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation at
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
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CC      or send an email to license@isb-sib.ch).

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RT "Odorant signal termination by olfactory UDP glucuronosyl
 RT transferase." :
 CC Nature 349:790-793(1991).
 CC -I- FUNCTION: UDPGT IS OF MAJOR IMPORTANCE IN THE CONJUGATION AND
 CC SUBSEQUENT ELIMINATION OF POTENTIALLY TOXIC XENOBIOTICS AND
 CC ENDOGENOUS COMPOUNDS. THIS ISOFORM IS ACTIVE ON ODORANTS AND
 CC SEEMS TO BE INVOLVED IN OLFACTION. IT COULD HELP CLEAR LIPOPHILIC
 CC ODORANT MOLECULES FROM THE SENSORY EPITHELIUM.
 CC -I- CATALYTIC ACTIVITY: UDP-GLUCURONATE + ACCEPTOR = UDP + ACCEPTOR
 CC BETA-D-GLUCOSONOSIDE.
 CC -I- TISSUE SPECIFICITY: OLFACTORY EPITHELIUM.
 CC -I- SIMILARITY: BELONGS TO THE UDP-GLYCOSYLTRANSFERASE FAMILY.
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 CC
 CC EMBL: X57565; -; NOT_ANNOTATED_CDS.
 CC InterPro: IPR002213; -;
 CC Pfam: PF00201; UDPGT; 1.
 CC PROSITE: PS00375; UDPGT; 1.
 CC Transferrase: Glycosyltransferase; Glycoprotein; Transmembrane; Signal;
 CC Multigene family; Microsome; Olfaction.
 CC SIGNAL 1 20
 CC CHAIN 21 527 UDP-GLUCURONOSYLTRANSFERASE 2A1.
 CC TRANSMEM 491 507 POTENTIAL.
 CC CARBOHYD 49 49 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC CARBOHYD 313 313 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC SEQUENCE 527 AA; 59915 MW; 6A32A9B56E8BDE CRC64;
 Query Match 60.4%; Score 1691.5; DB 1; Length 527;
 Best Local Similarity 61.5%; Pred. No. 5.3e-126;
 Matches 324; Conservative 69; Mismatches 113; Indels 21; Gaps 5;

DB 481 LSWFOYHSIDVIGFLLACMASAILLVKCOLFEVFORIGTKXKKRBD 527
 RESULT 6
 ID UDBK_MACFA STANDARD; PRT; 530 AA.
 AC 077649;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE UDP-GLUCURONOSYLTRANSFERASE 2B20 PRECURSOR, MICROSOMAL (EC 2.4.1.17)
 DE (UDPGT).
 GN UGT2B20.
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecinae; Macaca.
 OC NCBI_TaxID=9541;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver, and prostate;
 RA Barbier O., Belanger A., Hum D.W.;
 RT "Cloning and characterization of a simian UDP-glucuronosyltransferase
 RT enzyme, UGT2B20, a novel steroid conjugating protein.";
 RT Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 CC -I- FUNCTION: UDPGT IS OF MAJOR IMPORTANCE IN THE CONJUGATION AND
 CC SUBSEQUENT ELIMINATION OF POTENTIALLY TOXIC XENOBIOTICS AND
 CC ENDOGENOUS COMPOUNDS.
 CC -I- CATALYTIC ACTIVITY: UDP-GLUCURONATE + ACCEPTOR = UDP + ACCEPTOR
 CC BETA-D-GLUCOSONOSIDE.
 CC -I- SUBCELLULAR LOCATION: MICROSOMAL.
 CC -I- SIMILARITY: BELONGS TO THE UDP-GLYCOSYLTRANSFERASE FAMILY.
 CC
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 CC
 CC EMBL: AF072223; AAD08808.1; -;
 CC InterPro: IPR002213; -;
 CC Pfam: PF00201; UDPGT; 1.
 CC PROSITE: PS00375; UDPGT; 1.
 CC Transferrase: Glycosyltransferase; Glycoprotein; Transmembrane; Signal;
 CC Multigene family; Microsome.
 CC SIGNAL 1 23
 CC CHAIN 24 530 UDP-GLUCURONOSYLTRANSFERASE 2B20.
 CC TRANSMEM 495 515 POTENTIAL.
 CC CARBOHYD 65 65 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC CARBOHYD 103 103 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC CARBOHYD 316 316 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC CARBOHYD 483 483 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC SEQUENCE 530 AA; 61225 MW; A5EB47F8D517DBDA CRC64;
 Query Match 60.2%; Score 1686; DB 1; Length 530;
 Best Local Similarity 60.7%; Pred. No. 1.5e-125;
 Matches 321; Conservative 76; Mismatches 112; Indels 20; Gaps 5;

OX NCBI_TaxID=9606;
RN [1]
RN SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=90243659; PubMed=2159463;
RA Rittler J.K., Sheen Y.Y., Owens I.S.;
RT "Cloning and expression of human liver UDP-glucuronosyltransferase in COS-1 cells. 3,4-catechol estrogens and estriol as primary substrates.";
RT J. Biol. Chem. 265:7900-7906(1990).
RL
CC -1- FUNCTION: UDPGT IS OF MAJOR IMPORTANCE IN THE CONJUGATION AND SUBSEQUENT ELIMINATION OF POTENTIALLY TOXIC XENOBIOTICS AND ENDOGENOUS COMPOUNDS.
CC -1- FUNCTION: ITS UNIQUE SPECIFICITY FOR 3,4-CATECHOL ESTROGENS AND ESTRIOL SUGGESTS IT MAY PLAY AN IMPORTANT ROLE IN REGULATING THE LEVEL AND ACTIVITY OF THESE POTENT AND ACTIVE ESTROGEN METABOLITES.
CC -1- CATALYTIC ACTIVITY: UDP-GLUCURONATE + ACCEPTOR = UDP + ACCEPTOR
CC BETA-D-GLUCURONOSIDE.
CC -1- SUBCELLULAR LOCATION: MICROSOMAL.
CC -1- SIMILARITY: BELONGS TO THE UDP-GLYCOSYLTRANSFERASE FAMILY.
CC
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CC
CC EMBL: J05428; AAA36793.1; -
CC PIR: A35366; A35366.
DR DR
DR MIM: 600068; -
DR InterPro: IPR002213; -
DR Pfam: PF00201; UDPGT; 1.
DR PROSITE: PS00375; UDPGT; 1.
KW Transferase; Glycosyltransferase; glycoprotein; Transmembrane; Signal;
KW Multigene family; Microsome.
FT FT
FT STGNAL 1 23 BY SIMILARITY.
FT CHAIN 24 529 UDP-GLUCURONOSYLTRANSFERASE 2B7.
FT TRANSMEM 493 509 POTENTIAL.
FT CARBOHYD 67 67 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 68 68 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 315 315 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 529 AA; 60694 MW; 94B1CAGCE92F146 CRC64;

Query Match 59.8%; Score 1676.5; DB 1; Length 529;
Best Local Similarity 60.6%; Pred. No. 8,2e-125;
Matches 320; Conservative 67; Mismatches 138; Indels 3; Gaps 3;

DB 302 NGVVFSLGSMVSNMTEERANVIASALAOIPQKVLWRFEDGKPKDPTLGLNRLYKWIPOND 361
QY 360 LIGHPKTKARFTTGGNGGTEATYHGVPMGYPIFGDOLNIAHMKAGAVENFKMT 419
DB 362 LIGHPKTKARFTTGGANGITEATYHGVPMGYPIFGDOLNIAHMKAGAVENFKMTS 421
QY 420 SEDLLRLFRVITPSSYKEMAMRLSRILHDDPVPFLDRAVWIEFVRHKGAKHLRSAAH 479
DB 422 STDILNALKRVINDPSTKENYMKLSRIHQDPKVPFLDRAVWIEFVRHKGAKHLRVAAH 481
QY 480 DLTFWQYSIDVIGFLTCVATAFLFTKCFLESCQFENKTRKIEKE 527
DB 482 DLTFWQYSIDVIGFLTCVATAFLFTKCFLESCQFENKTRKIEKE 529

RESULT 9
ID DBE_RABIT STANDARD; PRT; 530 AA.
AC P36513;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE UDP-GLUCURONOSYLTRANSFERASE 2B14 PRECURSOR, MICROSOMAL (EC 2.4.1.17)
DE (UDPGT) (EGT12).
GN UGT2B14.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=NEW ZEALAND WHITE; TISSUE=Liver;
RX MEDLINE=93315511; PubMed=8325897;
RA Tukey R.H., Pendurthi U.R., Nguyen N.T., Green M.D., Tephly T.R.;
RT "Cloning and characterization of rabbit liver up- glucuronosyltransferase cDNAs. Developmental and inducible expression of 4-hydroxybiphenyl UGT2B13.";
RT J. Biol. Chem. 268:15260-15266(1993).
RL
CC -1- FUNCTION: UDPGT IS OF MAJOR IMPORTANCE IN THE CONJUGATION AND SUBSEQUENT ELIMINATION OF POTENTIALLY TOXIC XENOBIOTICS AND ENDOGENOUS COMPOUNDS.
CC -1- CATALYTIC ACTIVITY: UDP-GLUCURONATE + ACCEPTOR = UDP + ACCEPTOR
CC BETA-D-GLUCURONOSIDE.
CC -1- SUBCELLULAR LOCATION: MICROSOMAL.
CC -1- DEVELOPMENTAL STAGE: EXPRESSED PRIMARILY IN ADULT RABBITS.
CC -1- SIMILARITY: BELONGS TO THE UDP-GLYCOSYLTRANSFERASE FAMILY.
CC
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CC
CC EMBL: L01082; AAA18021.1; -
CC PIR: C47113; C47113.
DR DR
DR InterPro: IPR002213; -
DR Pfam: PF00201; UDPGT; 1.
DR PROSITE: PS00375; UDPGT; 1.
KW Transferase; Glycosyltransferase; glycoprotein; Transmembrane; Signal;
KW Multigene family; Microsome.
FT FT
FT STGNAL 1 24 BY SIMILARITY.
FT CHAIN 25 530 UDP-GLUCURONOSYLTRANSFERASE 2B14.
FT TRANSMEM 494 510 POTENTIAL.
FT CARBOHYD 134 134 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 316 316 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 530 AA; 60664 MW; CEAA4BF25B3CB35 CRC64;

Query Match 59.5%; Score 1668.5; DB 1; Length 530;
Best Local Similarity 58.2%; Pred. No. 3,5e-124;
Matches 310; Conservative 86; Mismatches 116; Indels 21; Gaps 4;


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Db      300 SSGEGVYVFISGSINSLTEERAVIASALQAPQKYLWRFESKKPMDLGSNRLXKIWI 359
Oy      356 PONDILGPRTKAFETTHGCMNGIYEAIHGVPMGVPIFGDOLNIAMKAKAAVEINF 415
Db      360 PONDILGPRTKAFETTHGCMNGIYEAIHGVPMGVPIFGDOLNIAMKAKAAVEINF 419
Oy      416 KTMSEDELLRLRVTYTSSYKENAMRLSRHHDPVKPLDRAVEFWLEFVRHKGAKHLR 475
Db      420 KTMSSADLLNLMLKTLYINDPSYKENAMLTSLRIHQDPKPLDRAVEFWLEFVRHKGAKHLR 479
Oy      476 SAAMDLMFEQHSIDVIGFLLCVATAIFFETKECFLSQCKFNKTRIEKE 527
Db      480 VAAHDLTWYQYHSLDVIGFLLCVATITTYLVKCLLYRVVLGAGKKRRD 531

RESULT 12
UDBA_HUMAN STANDARD; PRT; 528 AA.
AC P36537;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE UDP-GLUCURONOSYLTRANSFERASE 2B10 PRECURSOR, MICROSOMAL (EC 2.4.1.17)
DE (UDPGR).
GN UGT2B10.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Liver;
RC MEDLINE=93326164; PubMed=8333863;
RA Jin C.-J., Miners J.O., Lillywhite K.J., McKenzie P.I.;
RT "cDNA cloning and expression of two new members of the human liver UDP-glucuronosyltransferase 2B subfamily."
RL Biochem. Biophys. Res. Commun. 194:496-503(1993).
CC -1- FUNCTION: UDPGT IS OF MAJOR IMPORTANCE IN THE CONJUGATION AND SUBSEQUENT ELIMINATION OF POTENTIALLY TOXIC XENOBIOTICS AND ENDOGENOUS COMPOUNDS.
CC -1- CATALYTIC ACTIVITY: UDP-GLUCURONATE + ACCEPTOR = UDP + ACCEPTOR BETA-D-GLUCURONOSIDE.
CC -1- SUBCELLULAR LOCATION: MICROSOMAL.
CC -1- SIMILARITY: BELONGS TO THE UDP-GLYCOSYLTRANSFERASE FAMILY.
CC -----
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Cc -----
DR EMBL; X63359; CA444961.1; -.
DR PIR; JN0620; JN0620.
DR MM; 600070; -.
DR InterPro: IPR002213; -.
DR Pfam; PF00201; UDPGT_1.
DR PROSITE; PS00375; UDPGT; 1.
KW Transferase; Glycosyltransferase; glycoprotein; Transmembrane; Signal; Multigene family; Microsome.
FT SIGNAL 1
FT CHAIN 1 23 BY SIMILARITY.
FT TRANSMEM 24 528 UDP-GLUCURONOSYLTRANSFERASE 2B10.
FT CARBOHYD 492 512 POTENTIAL.
FT CARBOHYD 66 66 N-LINKED (GLCNAC. . . ) (POTENTIAL).
FT CARBOHYD 314 314 N-LINKED (GLCNAC. . . ) (POTENTIAL).
FT CARBOHYD 481 481 N-LINKED (GLCNAC. . . ) (POTENTIAL).
SQ SEQUENCE 528 AA; 60774 MW; 56BEA3DBC032C2E0 CRC64;

Query Match 58.4%; Score 1635.5; DB 1; Length 528;
Best Local Similarity 59.8%; Pred. No. 1,4e-121;

```

Matches	311;	Conservative	72;	Mismatches	134;	Indels	3;	Gaps	2
QY	11	LLIQL-FCVCGCGCGVLYVPCDMSHWLVNKVYLEELIVRGHEVYVLTSHKPSLIDYRKP	69						
Db	9	LLIQLSFYSSGSGCGVLYVAAEYSLMMNMKLTLLKLELYVRGHEVYVLTSSAATLFDPNDS	68						
QY	70	SAKFQVYVHNPQORTSENEIEFYDVA-LNVVLGSLWISQVVKINDFVYVIRGLKMKCS	127						
Db	69	STLKLVEYVYTSLKTKTEFENIMQLVKRLSEIQKDIYVLPSSQQLMALINDIIRNPKD	128						
QY	128	FYIYQITLMMKLOETNYDVMIDPVIPGDLMAELLAVPEVLTLRISVGNMERSCGLTPA	187						
Db	129	VYSNKKLMKLTQESRSDIYFADAYLPCGELLAELEFNIPEVYSHSFSPYSFERNHGFI	188						
QY	188	PLSYVVPVPTGTLDRMTFLYERKNSMLSLYLFHFYQIDYDHYHHWEELYSALGRPTLCT	247						
Db	189	PSYVYVWVSKSLSDQMTFERVKNMILYVLFYFWQIFEMKKMKWDQFYSYEVLRPTTLST	248						
QY	248	VGKAELIWLIRTYWDEFEPQYQPNFEVYVGLCKCPAKAPKEMENFVSSGSDGIYVSTL	307						
Db	249	MKRAIDWLRNSWNEKFEPRFLPNVDYFVGSLCKCPAKPLPKMEEFYVSSGNGVYVSTL	308						
QY	308	GSLFQWVPEKANIIATSAALQIPQVLYVRYKKKAKSTLTGANTRLYDWTIPQNDLGHPKTK	367						
Db	309	GSMVSMTEERANVATATAKIPQVLYVRFEDGNKPDALGINTRLKWKIPQNDLGHPKTKR	368						
QY	368	AEITFGMNGIETALYHGVYVNVGVPIFGQDNIIMAKAKGAAYEINRTWTSSEDLRAL	427						
Db	369	AEITFGAGNGIETALYHGPVYVIGLPIFDQPNIMAKAKGAAYVDRTMSITDLNAL	428						
QY	428	KRVITDSSYKKNAMLSRIHHQPYKPLDRAVFWLIEYVNRHKGAKHLRSAADLTWFOHY	487						
Db	429	KRVINDPSKKEIMLSRIHQDPYKPLDRAVFWLIEFWNRHKGAKHLRYAAHNLTWFOYH	488						
QY	488	SIDVIGFLITCAATAIPLFTKCFLESCQKFKTKRIEKE	527						
Db	489	SLDVIGFLITCAATVILFTITKCLCFEKFMRKPKRKKGRD	528						
RESULT 13									
UDBB_HUMAN	ID	UDBB_HUMAN	STANDARD;	PRT;	529	AA.			
AC	075310;								
DT	15-DEC-1998 (Rel. 37, Created)								
DT	15-DEC-1998 (Rel. 37, Last sequence update)								
DT	15-DEC-1998 (Rel. 37, Last annotation update)								
DE	UDP-GLUCURONOSYLTRANSFERASE ZB11 PRECURSOR, MICROSOMAL (EC 2.4.1.17) (UDPgt).								
GN	UGT2B11.								
OS	Homo sapiens (Human).								
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;								
OC	Mammalia; Euthera; Primates; Catarrhini; Hominiidae; Homo.								
OX	NCBI_TaxID=9606;								
RN	[1]								
RP	SEQUENCE FROM N.A.								
RX	MEDLINE=98340847; PubMed=9675083;								
RA	Beaulieu M., Levesque E., Hum D.W., Belanger A.;								
RT	"Isolation and characterization of a human orphan UDP-								
RL	glucuronosyltransferase, UGT2B11."								
CC	Biochem. Biophys. Res. Commun. 248:44-50(1998).								
CC	-FUNCTION: UDPGT IS OF MAJOR IMPORTANCE IN THE CONJUGATION AND								
CC	SUBSEQUENT ELIMINATION OF POTENTIALLY TOXIC XENOBIOTICS AND								
CC	ENDOGENOUS COMPOUNDS.								
CC	-1- CATALYTIC ACTIVITY: UDP-GLUCURONATE + ACCEPTOR = UDP + ACCEPTOR								
CC	BETA-D-GLUCURONOSIDE.								
CC	-1- SUBCELLULAR LOCATION: MICROSOMAL.								
CC	-1- TISSUE SPECIFICITY: WIDELY EXPRESSED.								
CC	-1- SIMILARITY: BELONGS TO THE UDP-GLYCOSYLTRANSFERASE FAMILY.								
CC	-----								
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration								
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CC	modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
CC	-----
CC	EMBL; AF016492; AAC27891.1; -
DR	MIM; 603064; -
DR	InterPro; IPR002213; -
DR	Pfam; PF00201; UDPGT. 1.
DR	PROSITE; PS00375; UDPGT. 1.
KW	Transferase; Glycosyltransferase; Glycoprotein; Transmembrane; Signal;
KW	MultiGene Family; Microsome.
FT	SIGNAL 1 21 POTENTIAL.
FT	CHAIN 22 529 UDP-GLUCONOSYLTRANSFERASE 2B11.
FT	TRANSMEM 493 513
FT	CARBOHYD 315 315 N-LINKED (GLUCANAC. . .) (POTENTIAL).
SQ	SEQUENCE 529 AA; 61038 MW; CEAC3C71CFC2AB4 CRC64;
Query Match	58.1%; Score 1628.5; DB 1; Length 529;
Best local Similarity	58.9%; Pred. No. 5e-121;
Matches 312; Conservative 71; Mismatches 128; Indels 19; Gaps 4;	
QY	9 VELLIDLCF-VGCGFCGKYLVPDCMSHLNLYKLTLEELIVRGHEVYVLTSHKPSLIDYR 67
DB	8 VLLLIHLSCYFSSGSCGKYLVAEYSHMMNKRTIKELVGRHEVYVLAASASILDPN 67
QY	68 KPSALKEFVHMHPDRTREENEFIVDALNVLPGSLTQWSYKLDNFV-----EI 117
DB	68 DASLTKFEYVPIPSLTKTEPNI-----IMQVKRW-SDIRKSFYWSQEOELIMEL 119
QY	118 KGLTKMCSFTIYNOTLKKLQETNYDVALIDPVIPCGDMAELLAVFVLTIRISVGN 177
DB	120 YDIFRNFCRDVYSNKKVMKKLOESRFIDVPADAVPCGELLALNLIRFVSLFTPTGYT 179
QY	178 MRSQSGKLPAPIASYPVPMVGTGIDPMFTLEVKKMSLSVLFHEHIODYDHFVEEYFSA 237
DB	180 IRRHSGGLFFPSTYPIYMSKLSIDQMTMEYKKNMIIYLYFDFMFQSDMKKMDQFYSEV 239
QY	238 IGRPTTLCEVGAKAIWLIRTYWDFEFPQAPOPNPEFEFGHLCRPAKALPREKMEFVQS 297
DB	240 IGRPTTLFETWKGADIMLRNMSWSQRFPHRLPVDVDFGFGHCRCAPRLPREMEFVQS 299
QY	298 GBDGIVNLSLGFONVTEEKANIIASLAOIPQVLMRYKKGKPSLGNRLYDWPQ 357
DB	300 GENGVAVFSLSVISNMFAERANVATLAKIPQVLMRFEDGNKPDALGINTRLYKWPQ 359
QY	358 NDLCHPKTKAFITFGGANGIYEALVHGVPMVGPVIGDOLDNIAHKKAGAVETNEKT 417
DB	360 NDLCHPKTKAFITFGGANGIYEALVHGVPMVGPVIGDOLDNIAHKKAGAVETNEKT 419
QY	418 MTSDDLALRLNTVITDSSYKENAKRLSRHHDDVPKPLDRAVFIETVFMRRKAKHLRSA 477
DB	420 MTSDDLALRLNTVINDPLRYKENIMKLSIQHDQVVKPLDRAVFIETVFMRRKAKHLRSA 479
QY	478 AHDLMFQHSIDVIGFLTCVATATLFLKGLFSQCKNKRKRIEKE 527
DB	480 AHDLMFQHSIDVIGFLTCVATATVITLTKFLCFPKFKRGGKGRKD 529
RESULT 14	
UDCL_RABIT	
ID	UDCL_RABIT STANDARD; PRT; 502 AA.
AC	P36514;
DT	01-JUN-1994 (Rel. 29, Created)
DT	01-JUN-1994 (Rel. 29, last sequence update)
DT	15-DEC-1998 (Rel. 37, last annotation update)
DE	UDP-GLUCONOSYLTRANSFERASE 2C1 MICROSOMAL (EC 2.4.1.17) (UDPGT)
DE	(FRAGMENT).
GN	UGR2C1 OR UGR2A2.
OS	Oryctolagus cuniculus (Rabbit).
OC	Eukaryota; Metazoa; Chordata; Cranialta; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
NCBI_TaxID=9986;	

```

RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN-NEW ZEALAND WHITE; TISSUE=Liver;
RA MEDLINE=93315511; PubMed=8325897;
RT Tukey R.H., Pendurthi U.R., Nguyen N.T., Green M.D., Teply T.R.;
RT "Cloning and characterization of rabbit liver UDP-
RT glucuronosyltransferase cDNAs. Developmental and inducible expression
RT of 4-hydroxydiphenyl UGT2B13."
RL J. Biol. Chem. 268:15260-15266(1993).
CC -1- FUNCTION: UDPGT IS OF MAJOR IMPORTANCE IN THE CONJUGATION AND
CC SUBSEQUENT ELIMINATION OF POTENTIALLY TOXIC XENOBIOTICS AND
CC ENDOGENOUS COMPOUNDS.
CC -1- CATALYTIC ACTIVITY: UDP-GLUCURONATE + ACCEPTOR = UDP + ACCEPTOR
CC BETA-D-GLUCURONOSIDE.
CC -1- SUBCELLULAR LOCATION: MICROSOMAL.
CC -1- SIMILARITY: BELONGS TO THE UDP-GLYCOSYLTRANSFERASE FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: L01083; AAA18023.1; -.
DR InterPro: IPR002213; -.
DR Pfam: PF00201; UDPGT. 1.
DR PROSITE: PS00375; UDPGT. 1.
KW Transferase; Glycosyltransferase; Glycoprotein; Transmembrane;
KW Multigene family; Microsome.
FT NON_TER 1
FT TRANSMEM 466 481 POTENTIAL.
FT CARBOHYD 177 177 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 288 288 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 502 AA; 57449 MW; B5E65670BFAED1D3 CAC64;

Query Match 57.8%; Score 1620; DB 1; Length 502;
Best Local Similarity 60.3%; Pred. No. 2.2e-120;
Matches 305; Conservative 85; Mismatches 98; Indels 18; Gaps 5;

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OY 502 AIFLTKCFESQKFNKTRKIERE 527
DB 477 IIFLAKCCLFFYRRCKTKGNKRRE 502

RESULT 15
UDBC_RAT
ID UDBC_RAT STANDARD: PRT: 530 AA.
AC P36511;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE UDP-GLUCURONOSYLTRANSFERASE 2B12 PRECURSOR, MICROSOMAL (EC 2.4.1.17)
DE (UDPGT).
DE UGT2B12.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxId=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN-SPRAGUE-DAWLEY; TISSUE=Liver, and Kidney;
RX MEDLINE=96032669; PubMed=7574722;
RA Jackson M.R., Clarke D.J., Oturu E.M., Styczynski P.B.,
RA Green M.R., Burchell B., Teply T.R.;
RT "Cloning and expression of a rat liver phenobarbital-inducible UDP-
RT glucuronosyltransferase (2B12) with specificity for monoterpenoid
RT alcohols."
RL Arch. Biochem. Biophys. 322:460-468(1995).
RL [2]
RP SEQUENCE OF 24-38, AND CHARACTERIZATION.
RX STRAIN-WISTAR; TISSUE=Liver;
RX MEDLINE=91312327; PubMed=1906977;
RA Styczynski P.B., Green M.S., Puig J., Coffman B.L., Teply T.R.;
RT "Purification and properties of a rat liver phenobarbital-inducible
RT 4-hydroxydiphenyl UDP-glucuronosyltransferase."
RL Mol. Pharmacol. 40:80-84(1991).
RL [3]
RP FUNCTION: UDPGT IS OF MAJOR IMPORTANCE IN THE CONJUGATION AND
RP SUBSEQUENT ELIMINATION OF POTENTIALLY TOXIC XENOBIOTICS AND
RP ENDOGENOUS COMPOUNDS. CATALYZES THE TRANSFER OF GLUCURONIC ACID
RP FROM UDP-GLUCURONIC ACID TO VARIOUS AGLYCONE MOLECULES. CATALYZES
RP THE GLUCURONIDATION OF MONOTERPENOID ALCOHOLS, SUCH AS (-)-
RP BORNEDIOL, (+)-MENTHOL, AND (-)-NOPOL. IN ADDITION, A NUMBER OF
RP SIMPLE PHENOLIC COMPOUNDS, SUCH AS HYDROXYDIPHENYLS, 7-
RP HYDROXYLATED COCAINANS, P-NITROPHENOL, AND FOOD-DERIVED SUBSTANCES
RP (E.G., MARINEGININ AND EUGENOL), AND 4-METHYLBELLIFERONE ARE ALSO
RP SUBSTRATES.
RL [4]
RP FUNCTION: UDPGT IS OF MAJOR IMPORTANCE IN THE CONJUGATION AND
RP SUBSEQUENT ELIMINATION OF POTENTIALLY TOXIC XENOBIOTICS AND
RP ENDOGENOUS COMPOUNDS. CATALYZES THE TRANSFER OF GLUCURONIC ACID
RP FROM UDP-GLUCURONIC ACID TO VARIOUS AGLYCONE MOLECULES. CATALYZES
RP THE GLUCURONIDATION OF MONOTERPENOID ALCOHOLS, SUCH AS (-)-
RP BORNEDIOL, (+)-MENTHOL, AND (-)-NOPOL. IN ADDITION, A NUMBER OF
RP SIMPLE PHENOLIC COMPOUNDS, SUCH AS HYDROXYDIPHENYLS, 7-
RP HYDROXYLATED COCAINANS, P-NITROPHENOL, AND FOOD-DERIVED SUBSTANCES
RP (E.G., MARINEGININ AND EUGENOL), AND 4-METHYLBELLIFERONE ARE ALSO
RP SUBSTRATES.
CC -1- CATALYTIC ACTIVITY: UDP-GLUCURONATE + ACCEPTOR = UDP + ACCEPTOR
CC BETA-D-GLUCURONOSIDE.
CC -1- SUBCELLULAR LOCATION: MICROSOMAL.
CC -1- TISSUE SPECIFICITY: LIVER. LOWER LEVELS SEEN IN THE KIDNEY AND
CC TESTIS.
CC -1- INDUCTION: BY PHENOBARBITAL.
CC -1- PYM: N-GLYCOSYLATED (PROBABLY).
CC -1- POLYMORPHISM: THE SEQUENCE SHOWN IS THAT OF THE LIVER ISOZYME.
CC -1- THE KIDNEY ISOFORMS DIFFERS IN 12 POSITIONS.
CC -1- SIMILARITY: BELONGS TO THE UDP-GLYCOSYLTRANSFERASE FAMILY.
CC -----
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CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U06273; AAA83404.1; -.
DR EMBL: U06274; AAA83405.1; -.
DR InterPro: IPR002213; -.
DR Pfam: PF00201; UDPGT. 1.
DR PROSITE: PS00375; UDPGT. 1.
KW Transferase; Glycosyltransferase; Glycoprotein; Transmembrane; Signal;

```

KW Multigene family; Microsome.
 FT SIGNAL 1 23
 FT CHAIN 24 530
 FT TRANSMEM 494 510
 FT CARBOHYD 316 316
 FT VARIANT 2 2
 FT VARIANT 61 61
 FT VARIANT 71 71
 FT VARIANT 95 95
 FT VARIANT 183 183
 FT VARIANT 346 346
 FT VARIANT 398 398
 FT VARIANT 414 415
 FT VARIANT 433 433
 FT VARIANT 475 475
 FT VARIANT 488 488
 SO SEQUENCE 530 AA: 61060 MW: D49313CE3BE5BDF CRC64;
 UDP-GLUCURONOSYLTRANSFERASE 2B12.
 POTENTIAL.
 N-LINKED (GLCNAC, .) (POTENTIAL).
 S-> P (IN KIDNEY).
 F-> S (IN KIDNEY).
 D-> H (IN KIDNEY).
 N-> S (IN KIDNEY).
 O-> K (IN KIDNEY).
 P-> T (IN KIDNEY).
 A-> G (IN KIDNEY).
 VE-> AT (IN KIDNEY).
 V-> D (IN KIDNEY).
 K-> L (IN KIDNEY).
 O-> L (IN KIDNEY).

Query Match 56.9%; Score 1595; DB 1; Length 530;
 Best Local Similarity 57.9%; Pred. No. 2.2e-118;
 Matches 307; Conservative 74; Mismatches 143; Indels 6; Gaps 3;

OY 3 SDKSALVELLLOL-PCVGGCGGCVLVWPCDMSHMLNVLVLEELIVRGHEVTLTHSKP 61
 DB 2 SKRWISALLLOISFCFKSGKCVLVWPMEXSHWNKIKITILEELVQKGEVTLRPSAF 61
 OY 62 SLIDYKPSALKFEVYHMDPTRENEIFVDLALNY---LPGLSTWQSVIKLNDFFVEI 117
 DB 62 VLDPRKETSCLKF-VTFPTSFSSHDLENFTFVNVWYELPRDCLSTFLYLODTIDEX 120
 OY 118 RGTLMKMCESFYIYNOTLMAKLOETNYDWMLIDPVIPCGDLMALLAVPVLTLRISVGN 177
 DB 121 SDYCLTVCKEAVSNQFMKIQESKDFVFSDAISPGCELIAELLQIPFLYSIRFSPGYT 180
 OY 178 MERSCGKLPAPLSYVPVPMPTGLDRTMTFLERYKNSMLSVLFHWIODYDHYHMEEFYSKA 237
 DB 181 IQOYIGVLPFPSPYPMIFSGLAGOMFLTERVHNMICMLYDFWFOJFREKKWDPPYSKT 240
 OY 238 IGRPTTLCETVGAKEIWLIRTYWDFEFPQPOVQNFEEVQGLHCKPAKALPKMENFVQSS 297
 DB 241 LGRPTTAEIMGKAMWMLIRSYWDLFPHPISPNVDYIGGLHCKPAKPLPKDIEDFVQSS 300
 OY 298 GEDGIVFSLGSLFQNVTEERKANIISALAOIPQKVLWRKYGKRSSTIGANTRLYDWIPQ 357
 DB 301 GEHGVVPSLSGSMVANNMTEERKANIIMALAOIPQKVLWRFDGKRPPTLGPNTRLYKWLPO 360
 OY 358 NDLLGHPRTKAFITHGANGIYEALYHGVPMWGPVIFGDOLDNIAMKAKGAAYEINFRT 417
 DB 361 NDLLGHPRTKAFITHGANGIYEALYHGIPIGIPLFAEQHDNINAMVAKGAAYEVNFT 420
 OY 418 MTSDDLALALTVLITDSSYKENAMRLSRHHDPYKPLDRAVFWTEFYWRHKGAKHLRSA 477
 DB 421 MSKSDLLALAEVDINPFYKKNAMWLSIHHDPKPLDRAVFWTEFYWRHKGAKHLRSL 480
 OY 478 AHDLTWFOHYSIDVIGFLTCVATAIFLTKCFSCOKFNKTRIEKRE 527
 DB 481 GHNLPMWQYHSLDVIIGFLSCVAATVVALKCFLEFYRFFVKKKKTKNE 530

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